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A site-specific curated database for the microorganisms of activated sludge and anaerobic digesters

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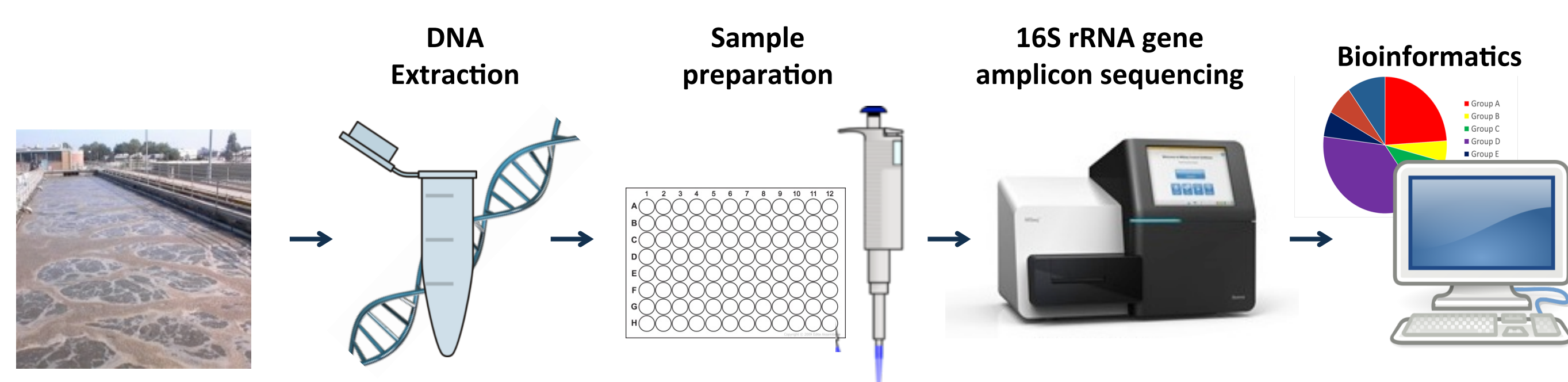
A site-specific curated database for the microorganisms of activated sludge and anaerobic digesters

Simon J. McIlroy, Rasmus H. Kirkegaard, Bianca McIlroy, Marta Nierychlo, Jannie M. Kristensen, Søren M. Karst, Mads Albertsen and Per H. Nielsen

Standard 16S rRNA protocols

Amplicon sequencing of the 16S rRNA gene now allows high throughput analyses and monitoring of the whole microbial communities of wastewater treatment systems.

However, meaningful cross study comparisons are hindered by the substantial influence of the selected DNA extraction method, PCR primers and reference taxonomy.

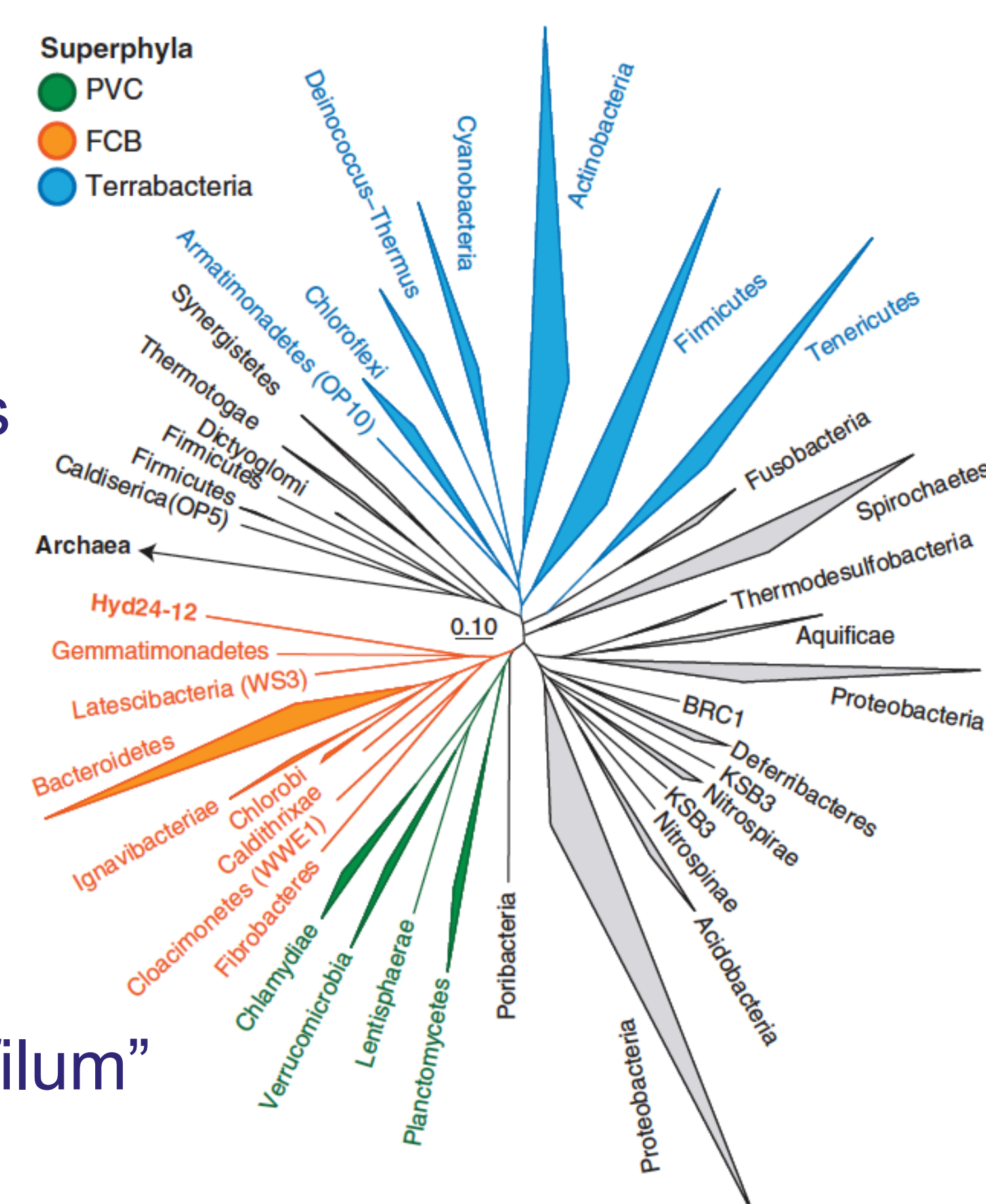


MiDAS¹ provides protocols for DNA extraction, 16S rRNA gene amplicon library preparation² and bioinformatic analysis – all optimised for application to wastewater treatment system samples.

Curated site-specific taxonomy

Reliable function prediction for phylotypes requires taxonomic assignment to the species or genus level.

Many of the abundant activated sludge and anaerobic digester organisms have no cultured representatives and are not annotated in popular public databases applied for taxonomic assignment. i.e. the uncultured fermentative bulking filament “*Ca. Promineofilum*” (0092 morphotype).

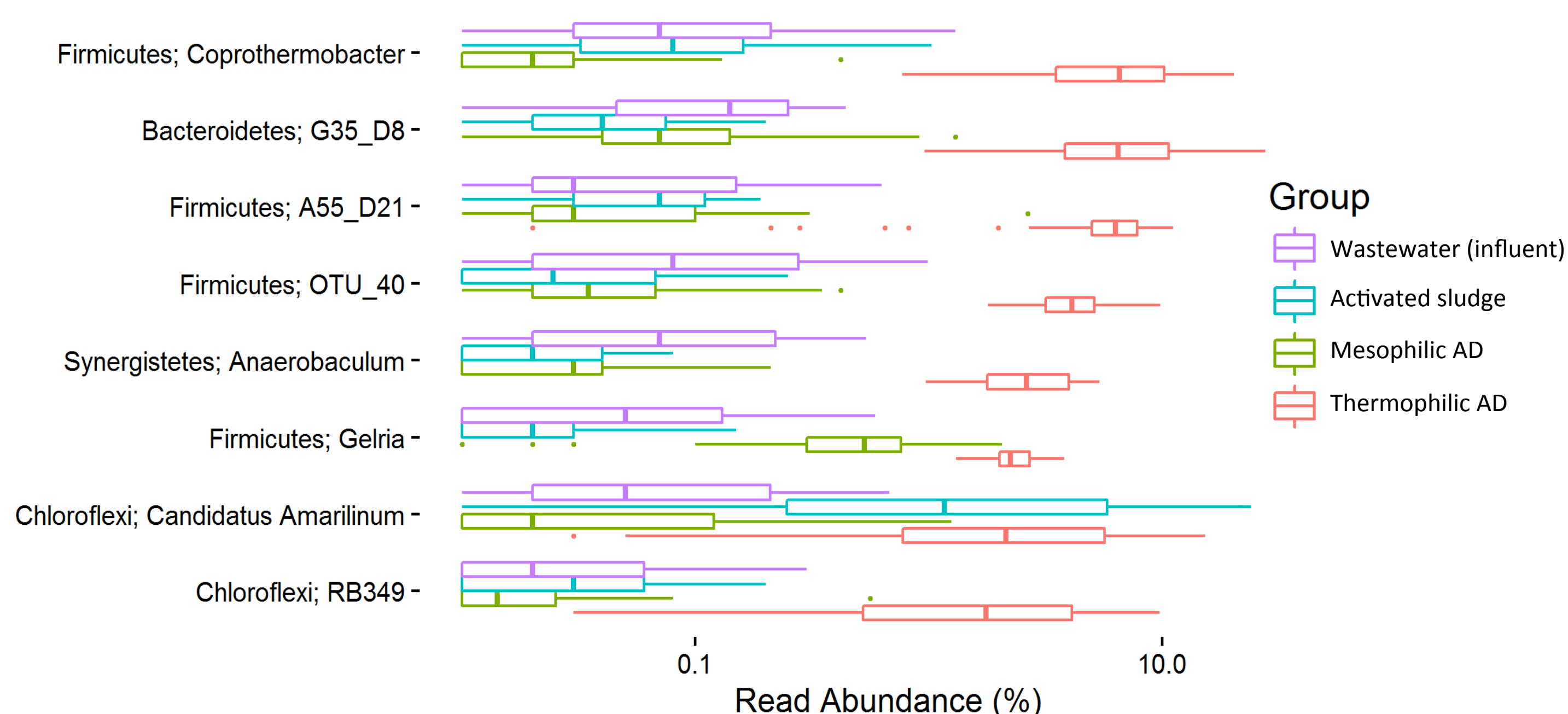


MiDAS provides a site-specific taxonomic database curated for the organisms of wastewater treatment systems.

www.midasfieldguide.org

Distribution

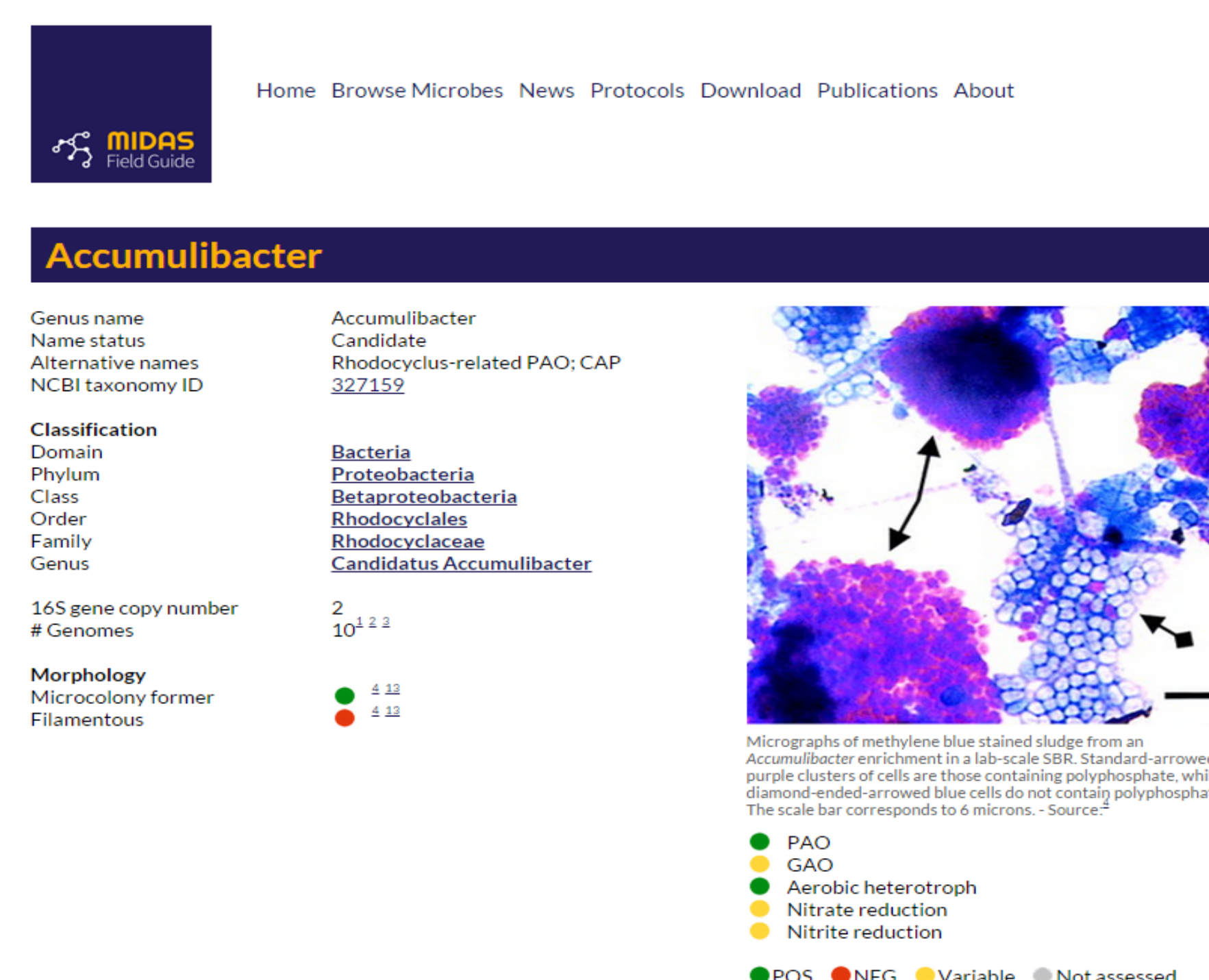
Large scale surveys of the microbial communities of wastewater treatment systems incl. >50 full-scale systems over several years.



MiDAS includes abundance values for influent wastewater, activated sludge and anaerobic digester (AD) – identifying abundant phylotypes and giving an insight into migration. An important example being the link between foaming episodes in anaerobic digesters and migration of “*Ca. Microthrix* spp.” from activated sludge.

Linking identity with function

The online **MiDAS field guide** provides profiles for all abundant and process important phylotypes - linking their identity to current information on their morphology, physiology and distribution. This currently includes profiles for >300 bacterial and 8 archaeal genus level taxa.



MiDAS is intended as a collaborative resource for all interested in the biotechnologically important fields of wastewater treatment and biogas production.

¹ McIlroy et al. (2015) MiDAS: the field guide to the microbes of activated sludge. *Database*. 2015, bav062.

² Albertsen et al. (2015) Back to basics – the influence of DNA extraction and primer choice on phylogenetic analysis of activated sludge communities. *PLoS ONE* 10. e0132783.